

FIG 1

5' 11 20 29 38 47 56
 GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG GCA

 65 74 83 92 101 110
 GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT AAC AGC

 119 128 137 146 155 164
 AAG ATG GCT TTG AAC TCA GGG TCA CCA CCA GCT ATT GGA CCT TAC TAT GAA AAC

 M A L N S G S P P A I G P Y Y E N

 173 182 191 200 209 218
 CAT GGA TAC CAA CCG GAA AAC CCC TAT CCC GCA CAG CCC ACT GTG GTC CCC ACT

 H G Y Q P E N P Y P A Q P T V V P T

 227 236 245 254 263 272
 GTC TAC GAG GTG CAT CCG GCT CAG TAC TAC CCG TCC CCC GTG CCC CAG TAC GCC

 V Y E V H P A Q Y Y P S P V P Q Y A

 281 290 299 308 317 326
 CCG AGG GTC CTG ACG CAG GCT TCC AAC CCC GTC GTC TGC ACG CAG CCC AAA TCC

 P R V L T Q A S N P V V C T Q P K S

 335 344 353 362 371 380
 CCA TCC GGG ACA GTG TGC ACC TCA AAG ACT AAG AAA GCA CTG TGC ATC ACC TTG

 P S G T V C T S K T K K A L C I T L

 389 398 407 416 425 434
 ACC CTG GGG ACC TTC CTC GTG GGA GCT GCG CTG GCC GCT GGC CTA CTC TGG AAG

 T L G T F L V G A A L A A G L L W K

 443 452 461 470 479 488
 TTC ATG GGC AGC AAG TGC TCC AAC TCT GGG ATA GAG TGC GAC TCC TCA GGT ACC

 F M G S K C S N S G I E C D S S G T

 497 506 515 524 533 542
 TGC ATC AAC CCC TCT AAC TGG TGT GAT GGC GTG TCA CAC TGC CCC GGC GGG GAG

 C I N P S N W C D G V S H C P G G E

 551 560 569 578 587 596
 GAC GAG AAT CGG TGT GTT CGC CTC TAC GGA CCA AAC TTC ATC CTT CAG GTG TAC

 D E N R C V R L Y G P N F I L Q V Y

 605 614 623 632 641 650
 TCA TCT CAG AGG AAG TCC TGG CAC CCT GTG TGC CAA GAC GAC TGG AAC GAG AAC

 S S Q R K S W H P V C Q D D W N E N

 659 668 677 686 695 704
 TAC GGG CGG GCG GCC TGC AGG GAC ATG GGC TAT AAG AAT AAT TTT TAC TCT AGC

 Y G R A A C R D M G Y K N N F Y S S

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1415	1424	1433	1442	1451	1460
GGG AAC GTC GAT TCT TGC CAG GGT GAC AGT GGA GGG CCT CTC GTC ACT TCG AAG					
-----	-----	-----	-----	-----	-----
G N V D S C Q G D S G G P L V T S K					
1469	1478	1487	1496	1505	1514
AAC AAT ATC TGG TGG CTG ATA GGG GAT ACA AGC TGG GGT TCT GGC TGT GCC AAA					
-----	-----	-----	-----	-----	-----
N N I W W L I G D T S W G S G C A K					
1523	1532	1541	1550	1559	1568
GCT TAC AGA CCA GGA GTG TAC GGG AAT GTG ATG GTA TTC ACG GAC TGG ATT TAT					
-----	-----	-----	-----	-----	-----
A Y R P G V Y G N V M V F T D W I Y					
1577	1586	1595	1604	1613	1622
CGA CAA ATG AGG GCA GAC GGC TAA TCC ACA TGG TCT TCG TCC TTG ACG TCG TTT					
-----	-----	-----	-----	-----	-----
R Q M R A D G *					
1631	1640	1649	1658	1667	1676
TAC AAG AAA ACA ATG GGG CTG GTT TTG CTT CCC CGT GCA TGA TTT ACT CTT AGA					
-----	-----	-----	-----	-----	-----
1685	1694	1703	1712	1721	1730
GAT GAT TCA GAG GTC ACT TCA TTT TTA TTA AAC AGT GAA CTT GTC TGG CAA AAA					
-----	-----	-----	-----	-----	-----
1739					
AAA AAA AAA A 3'					

002120" 55251960

FIG 2

1 gtcatatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg
 61 ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaacccat ggataccaac
 121 cggaaaaccc ctatcccgca cagcccactg tggccccac tgtctacgag gtgcatcccg
 181 ctccagtacta cccgtccccc gtgcccaggt acgccccgag ggtcctgacg caggcttcca
 241 accccgctgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta
 301 agaaagcact gtgcatcacc ttgaccttgg ggaccttcc tctggggagct gcgctggccg
 361 ctggcctact ctggaagtgc atgggcagca agtgctccaa ctctgggata gagtgcgact
 421 cctcagggtac ctgcatcaac cctctaaact ggtgtgatgg cgtgtcacac tgccccggcg
 481 gggaggacga gaatcggtgt gttcgctctt acggaccaa cttcatcctt cagatgtact
 541 catctcagag gaagtccctg caccctgtgt gccaaagacga ctggaacgag aactacgggc
 601 gggcgccctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg
 661 atgacagcgg atccaccagc tttatgaaac tgaacacaag tgccggcaat gtcgatatct
 721 ataaaaaact gtaccacagt gatgcctgtt cttcaaaagc agtgggtttct ttacgctgtt
 781 tagcctgcgg ggtcaacttg aactcaagcc gccagagcag gatcgtgggc ggtgagagcg
 841 cgctcccggg ggctggccc tggcagggtca gcctgcacgt ccagaacgtc cacgtgtgcg
 901 gaggtcccat catcaccccc gagtggatcg tgacagccgc cactgctgtg gaaaaacctc
 961 ttaacaatcc atggcatttg acggcatttg cggggatttt gagacaatct ttcattgtct
 1021 atggagccgg ataccaagta caaaaagtga tttctcatcc aaattatgac tccaagacca
 1081 agaacaatga cattgcgctg atgaagctgc agaagcctct gactttcaac gacctagtga
 1141 aaccagtgtg tctgccaac ccaggcatga tgctgcagcc agaacagctc tgctggattt
 1201 ccgggtgggg ggccaccgag gagaaaggga agacctcaga agtgtgaac gctgccagg
 1261 tgcttctcat tgagacacag agatgcaaca gcagatatgt ctatgacaac ctgatcacac
 1321 cagccatgat ctgtgccggc ttctgcagg ggaacgtcga ttcttgccag ggtgacagt
 1381 gagggcctct ggtcacttcg aacaacaata tctggtggct gataggggat acaagctggg
 1441 gttctggctg tgccaaagct tacagaccag gagtgtacgg gaatgtgatg gtattcacgg
 1501 actggattta tcgacaaatg aaggcaaacg gctaattccac atggtcttcg tctttgacgt
 1561 cgtttttaca gaaaacaatg gggctggttt tgcttccccg tgcattgatt actcttagag
 1621 atgattcaga ggtcacttca tttttattaa acagtgaact tgtctggctt tggcactctc
 1681 tgccatactg tgcaggtctg agtggctccc ctgcccagcc tgcctctcct aacctcttgt
 1741 ccgcaagggg tgatggccgg ctggttgttg gcaactggcg tcaatttgtg aaggaagagg
 1801 gttggaggct gccccattg agatcttcct gctgagtcct ttccaggggc caattttgga
 1861 tgagcatgga gctgtcactt ctgagctgct ggatgacttg agatgaaaaa ggagagacat
 1921 ggaaggaggag acagccaggt ggcacctgca gcggctgccc tctggggcca ctgtgtagt
 1981 tccccagcct acttcacaag gggattttgc tgatgggttc ttagagcctt agcagcctg
 2041 gatggtggcc agaaataaag ggaccagccc ttcattgggtg gtgacgtggt agtcaactgt
 2101 aaggggaaca gaaacatttt tgttcttatg gggtgagaat atagacagt cccttggtgc
 2161 gagggaagca attgaaaagg aacttgccct gagcactcct ggtgcaggtc tccacctgca
 2221 cattgggtgg ggctcctggg agggagactc agccttccct ctcactcctc ctgacctgc
 2281 tcctagcacc ctggagagtg aatgcccctt ggtcccctgg agggcgccaa gtttggcacc
 2341 atgtcggcct cttcaggcct gatagtcatt ggaaattgag gtccatgggg gaaatcaagg
 2401 atgctcagtt taagggtacac tgtttccatg ttatgtttct acacattgat ggtgggtgacc
 2461 ctgagttcaa agccatctt

ORF AMINO ACID SEQUENCE

MALNSGSPPAIGPYYNHGYQPENPYPAQPTVVPTVYEVHQAQYYPSVPVQYAPRVLTQASNPVVCTQPKSPSGTV
 CTSKTKKALCITLTLGTLVGAALAAGLLWKFMGSKCSNSGIECDSSGTCINPSNWCDGVSHCPGGEDENRCVRLY
 GPNFILQMYSSQRKSWHPVCQDDWNENYGRAACRDMGYKNNFYSSQGI VDDSGSTSFMKLNLSAGNVDIYKKLYHS
 DACSSKAVVSLRCLACGVNLNSSRQSRIVGGESALPGAWPQVSLHVQNVHVCSSII TPWEIVTAHCVEKPLNN
 PWHWTAFAGILRQSFMYGAGYQVQKVI SHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCW
 ISGWGATEEKGKTSEVLNAKVLIIETQRCNSRYVDNLITPAMICAGFLQGNVDSQGDSSGGLVTSNNNIWWLI
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09545285.04200

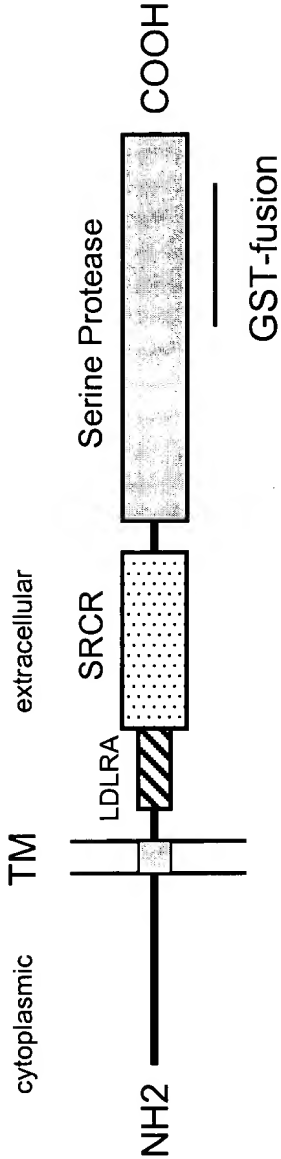
CAA	GGA	ATA	GTG	GAT	GAC	AGC	GGA	TCC	ACC	AGC	TTT	ATG	AAA	CTG	AAC	ACA	AGT
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Q	G	I	V	D	D	S	G	S	T	S	F	M	K	L	N	T	S
GCC	GGC	AAT	GTC	GAT	ATC	TAT	AAA	AAA	CTG	TAC	CAC	AGT	GAT	GCC	TGT	TCT	TCA
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A	G	N	V	D	I	Y	K	K	L	Y	H	S	D	A	C	S	S
AAA	GCA	GTG	GTT	TCT	TTA	CGC	TGT	ATA	GCC	TGC	GGG	GTC	AAC	TTG	AAC	TCA	AGC
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K	A	V	V	S	L	R	C	I	A	C	G	V	N	L	N	S	S
CGC	CAG	AGC	AGG	ATT	GTG	GGC	GGC	GAG	AGC	GCG	CTC	CCG	GGG	GCC	TGG	CCC	TGG
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R	Q	S	R	I	V	G	G	E	S	A	L	P	G	A	W	P	W
CAG	GTC	AGC	CTG	CAC	GTC	CAG	AAC	GTC	CAC	GTG	TGC	GGA	GGC	TCC	ATC	ATC	ACC
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Q	V	S	L	H	V	Q	N	V	H	V	C	G	G	S	I	I	T
CCC	GAG	TGG	ATC	GTG	ACA	GCC	GCC	CAC	TGC	GTG	GAA	AAA	CCT	CTT	AAC	AAT	CCA
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P	E	W	I	V	T	A	A	H	C	V	E	K	P	L	N	N	P
TGG	CAT	TGG	ACG	GCA	TTT	GCG	GGG	ATT	TTG	AGA	CAA	TCT	TTC	ATG	TTC	TAT	GGA
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W	H	W	T	A	F	A	G	I	L	R	Q	S	F	M	F	Y	G
GCC	GGA	TAC	CAA	GTA	GAA	AAA	GTG	ATT	TCT	CAT	CCA	AAT	TAT	GAC	TCC	AAG	ACC
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A	G	Y	Q	V	E	K	V	I	S	H	P	N	Y	D	S	K	T
AAG	AAC	AAT	GAC	ATT	GCG	CTG	ATG	AAG	CTG	CAG	AAG	CCT	CTG	ACT	TTC	AAC	GAC
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K	N	N	D	I	A	L	M	K	L	Q	K	P	L	T	F	N	D
CTA	GTG	AAA	CCA	GTG	TGT	CTG	CCC	AAC	CCA	GGC	ATG	ATG	CTG	CAG	CCA	GAA	CAG
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L	V	K	P	V	C	L	P	N	P	G	M	M	L	Q	P	E	Q
CTC	TGC	TGG	ATT	TCC	GGG	TGG	GGG	GCC	ACC	GAG	GAG	AAA	GGG	AAG	ACC	TCA	GAA
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L	C	W	I	S	G	W	G	A	T	E	E	K	G	K	T	S	E
GTG	CTG	AAC	GCT	GCC	AAG	GTG	CTT	CTC	ATT	GAG	ACA	CAG	AGA	TGC	AAC	AGC	AGA
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V	L	N	A	A	K	V	L	L	I	E	T	Q	R	C	N	S	R
TAT	GTC	TAT	GAC	AAC	CTG	ATC	ACA	CCA	GCC	ATG	ATC	TGT	GCC	GGC	TTC	CTG	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y	V	Y	D	N	L	I	T	P	A	M	I	C	A	G	F	L	Q

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FIG 3A

1	15 16	30 31	45 46	60 61	75 76	90	
	25	35	45	55	65	75	
GTC1	MALNSGPPAIGPY	ENHGYQENPYPAQ	TVPPTVYEVHPAQY	PSVPQYAPRVLTOA	SNPVVCTQPKSPSGT	VCTSKTKKALCITLT	90
TMPRSS2	MALNSGPPAIGPY	ENHGYQENPYPAQ	TVPPTVYEVHPAQY	PSVPQYAPRVLTOA	SNPVVCTQPKSPSGT	VCTSKTKKALCITLT	90
	91	105 106	120 121	135 136	150 151	165 166	180
GTC1	LGTFVLGAALAAAGLL	WKFMGSKCSNSGIEC	DSSGTCINPSNWC	VSHCPGGEDENRCVR	LYGNFILQ	WYSSQR	KSWHPVCQDDWNENY
TMPRSS2	LGTFVLGAALAAAGLL	WKFMGSKCSNSGIEC	DSSGTCINPSNWC	VSHCPGGEDENRCVR	LYGNFILQ	WYSSQR	KSWHPVCQDDWNENY
	181	195 196	210 211	225 226	240 241	255 256	270
GTC1	GRAACRDMGYKNNFY	SSQGIIVDDSGSTFSM	KLNTSAGNVDIYKKL	YHSDACSSKAVVSLR	CLACGVNLSNRQSR	IVGESALPGAWPWQ	270
TMPRSS2	GRAACRDMGYKNNFY	SSQGIIVDDSGSTFSM	KLNTSAGNVDIYKKL	YHSDACSSKAVVSLR	CLACGVNLSNRQSR	IVGESALPGAWPWQ	270
	271	285 286	300 301	315 316	330 331	345 346	360
GTC1	VSLHVQNVHVCGGSI	ITPEWIVTAAHCVEK	PLNPNHWTAFAGIL	RQSFMYGAGYQVQK	VISHPNYDSKTKNND	IALMKLQKPLTFNDL	360
TMPRSS2	VSLHVQNVHVCGGSI	ITPEWIVTAAHCVEK	PLNPNHWTAFAGIL	RQSFMYGAGYQVQK	VISHPNYDSKTKNND	IALMKLQKPLTFNDL	360
	361	375 376	390 391	405 406	420 421	435 436	450
GTC1	VKPVCLPNPGMMLQP	EQLCWISGWGATEEK	GKTSEVLNAAKVLLI	ETQRCNSRYVVDNLI	TPAMICAGFLQGNVD	SCQGDGSGPLVTSNN	450
TMPRSS2	VKPVCLPNPGMMLQP	EQLCWISGWGATEEK	GKTSEVLNAAKVLLI	ETQRCNSRYVVDNLI	TPAMICAGFLQGNVD	SCQGDGSGPLVTSNN	450
	451	465 466	480 481				
GTC1	NIWWLIGTWSGSGC	AKAYRPGVYGNVMVF	TDWIYRQMKANG				
TMPRSS2	NIWWLIGTWSGSGC	AKAYRPGVYGNVMVF	TDWIYRQMKANG				

FIG 3B



Cytoplasmic domain: a.a. 1-84
Protease domain: a.a. 255-492
SRCR domain: a.a. 149-242
LDLRA domain: a.a. 113-148
TM domain: a.a. 84-106
GST-fusion: a.a. 362-440

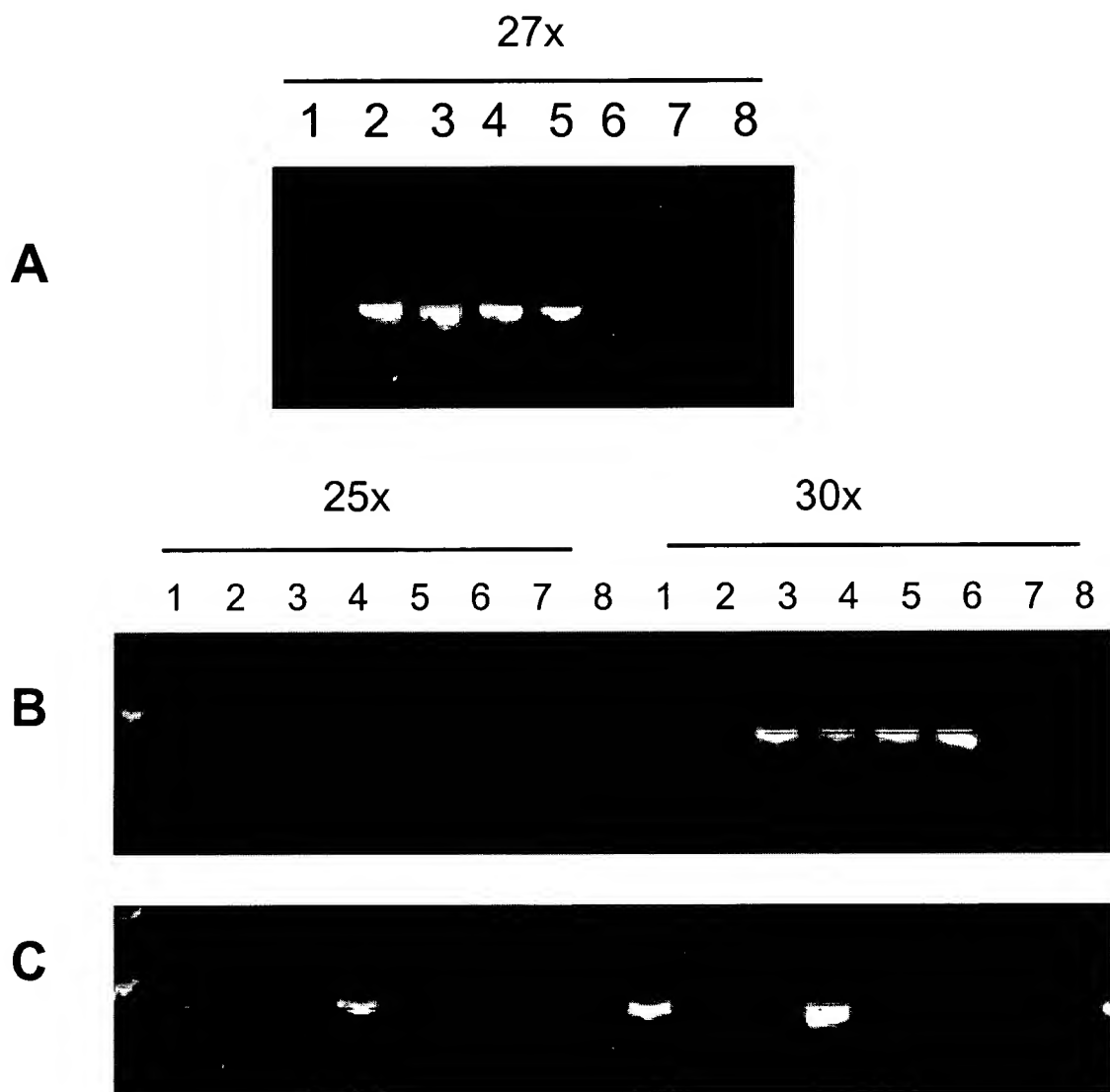
FIG 4

GATCTTCCTGCTGAGTCCTTTCCAGGGGCCAATTTTGGATGAGCATGGAGCTGTCACCTCTCAGCTGCTGGATGAC
TTGAGATGAAAAAGGAGAGACATGGAAAGGGAGACAGCCAGGTGGCACCTGCAGCGGCTGCCCTCTGGGGCCACTT
GGTAGTGTCCTCAGCCTACCTCTCCACAAGGGGATTTGCTGATGGGTTCCTANAGCCTTAGCAGCCCTGGATGGT
GGCCAGAAATAAAGGGACCAGCCCTTCATGGGTGGTGACGTGGTANTCACTTGTAAAGGGGAACAGAAACATTTTG
TTCTTATGGGGTGAGAATATAGACAGTGCCCTTGGTGCGAGGGAAGCAATTGAAAAGGAACTTGCCCTGAGCACTC
CTGGTGCA

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09615335.071200

FIG. 5



A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

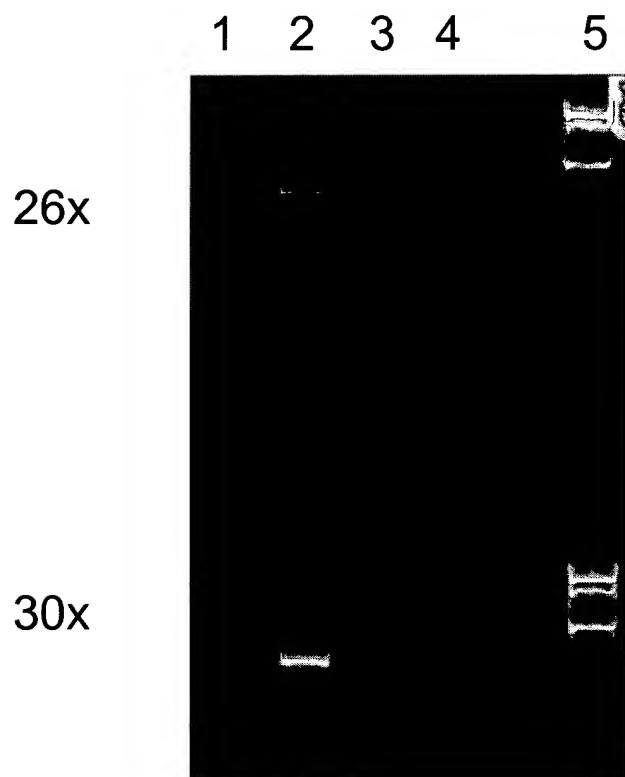
B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG 5D



- Prostate tumor pool
- Bladder tumor pool
- HeLa
- H2O
- Markers

FIG. 6

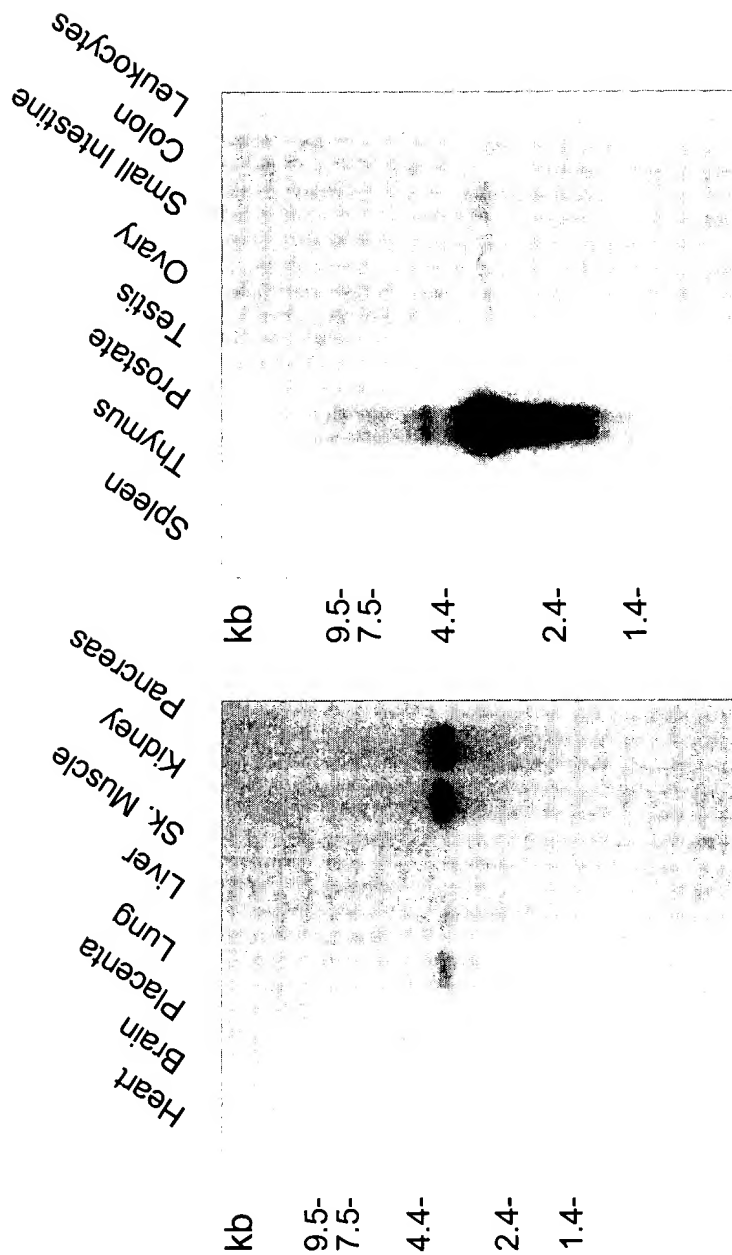


FIG. 7

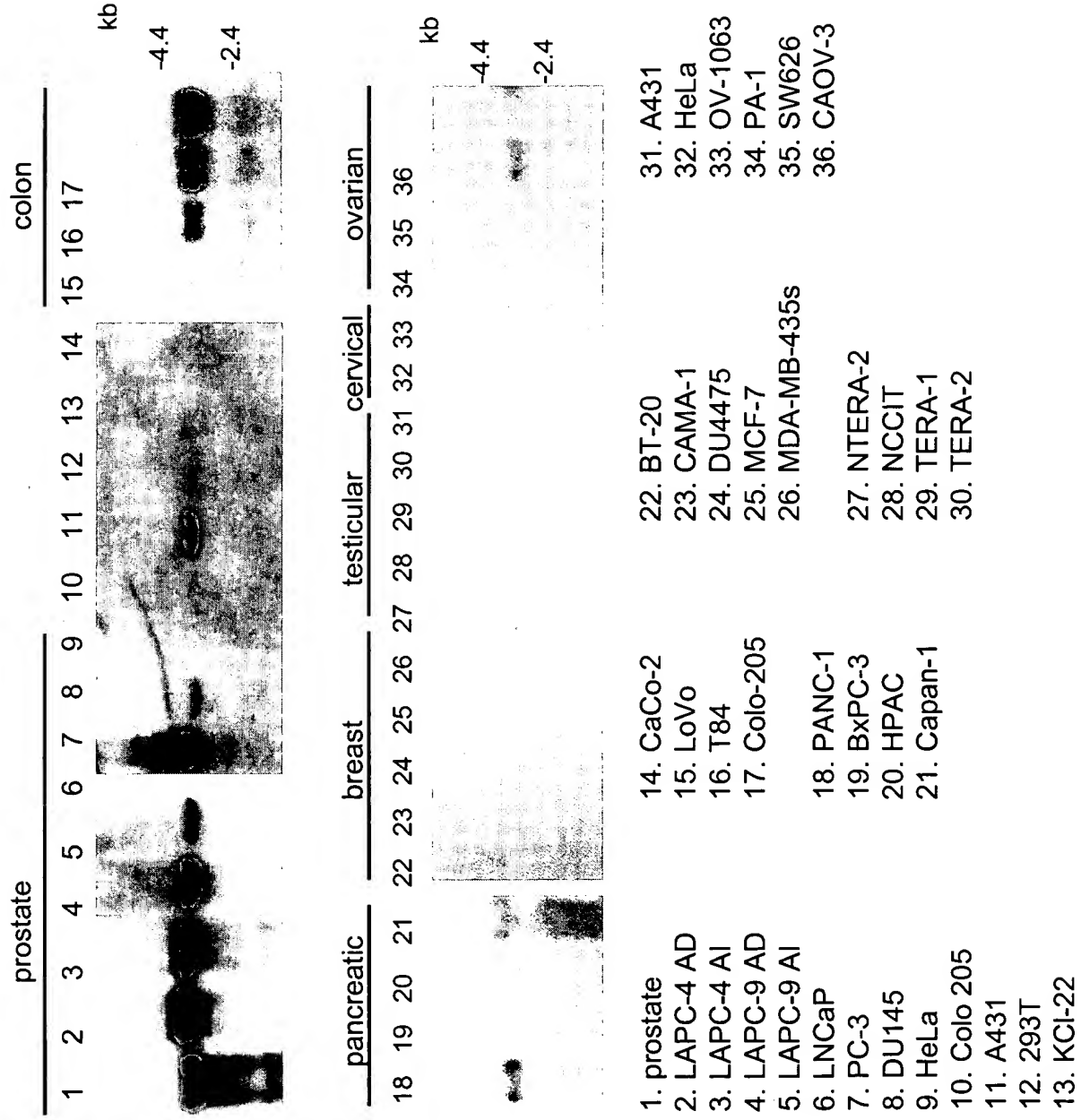


FIG. 8

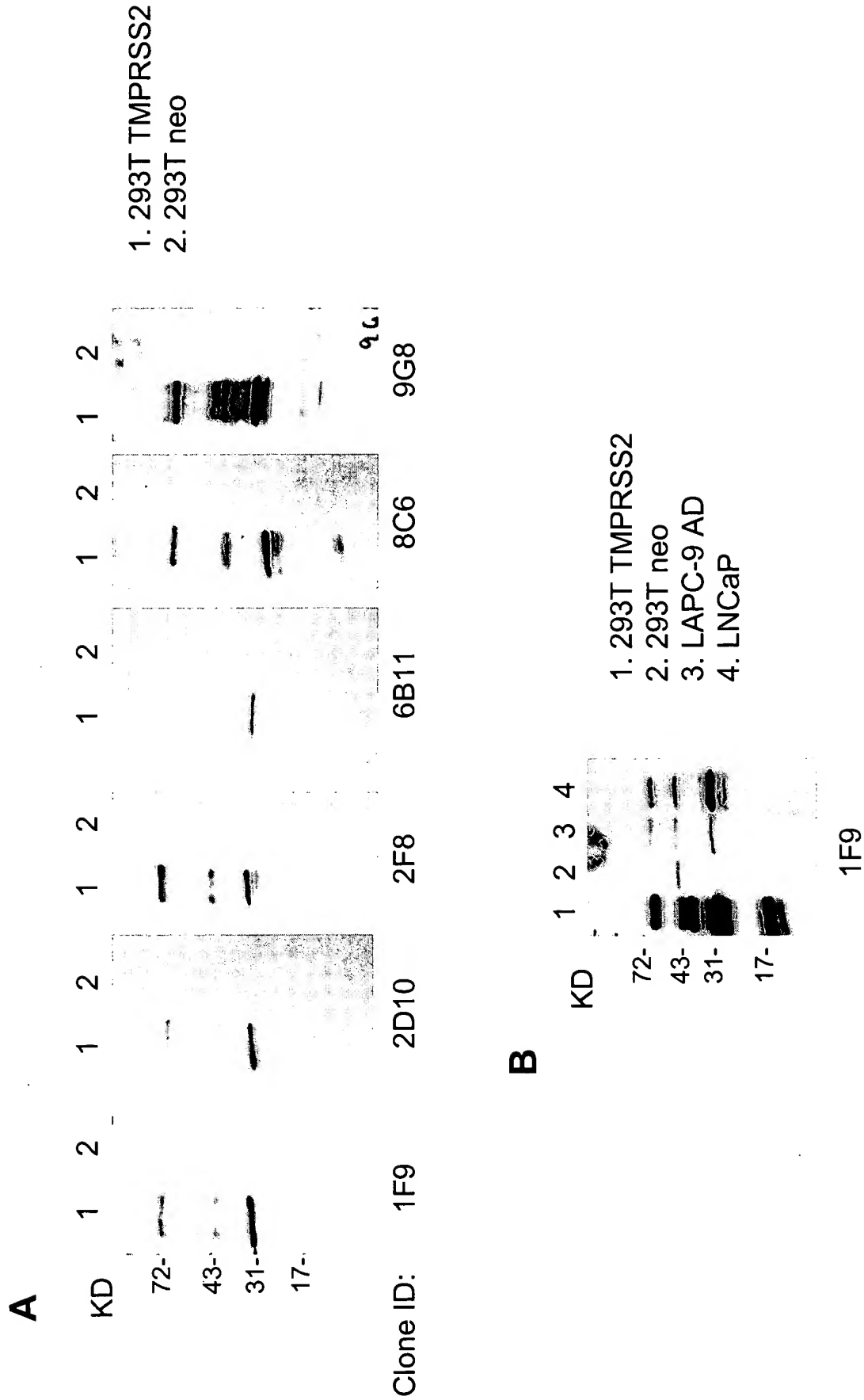
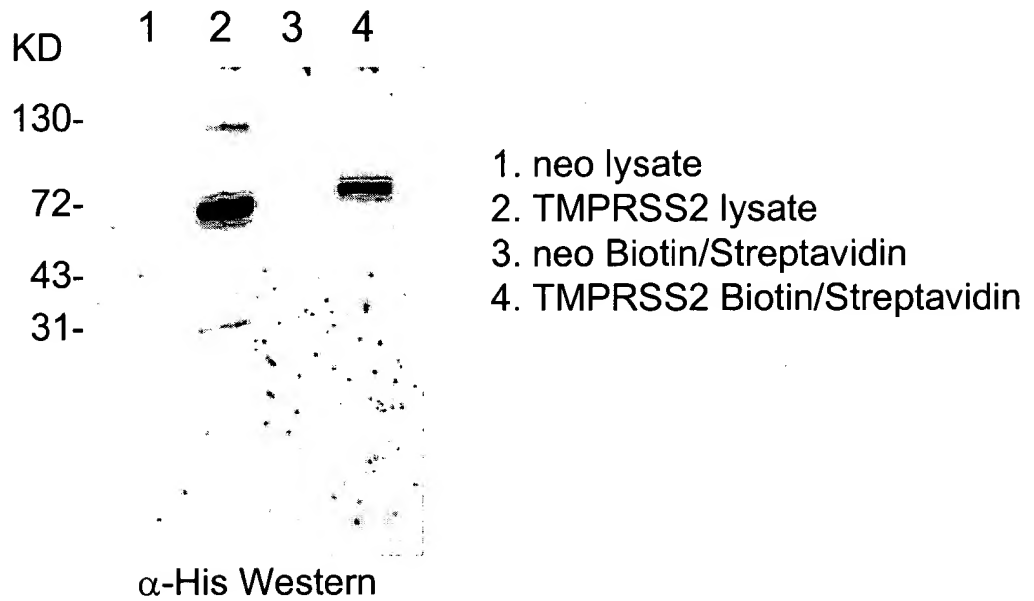


FIG. 9

A. In transfected 293T cells:



B. In prostate cancer cells:

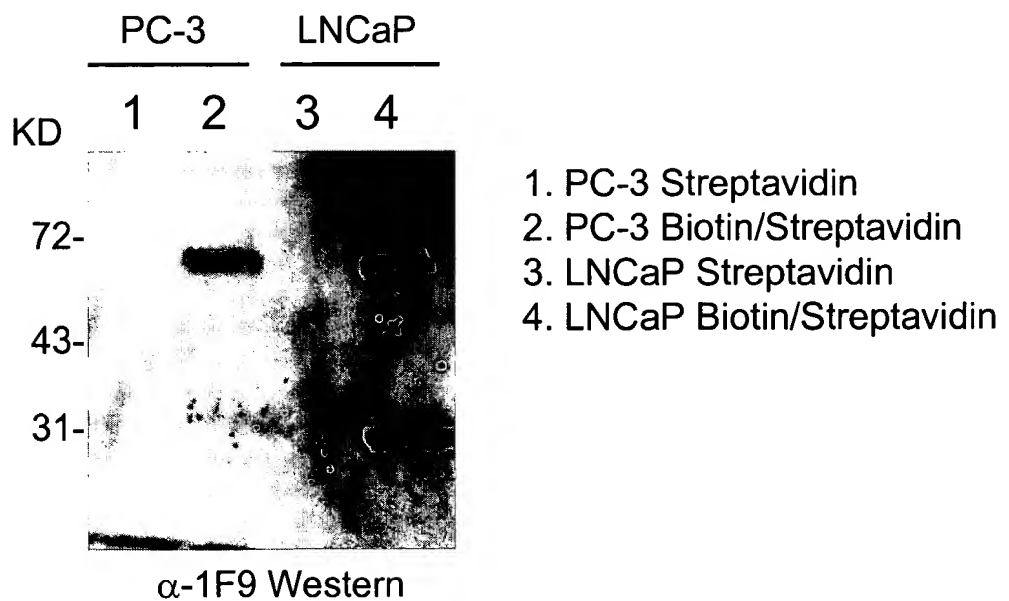


FIG. 10

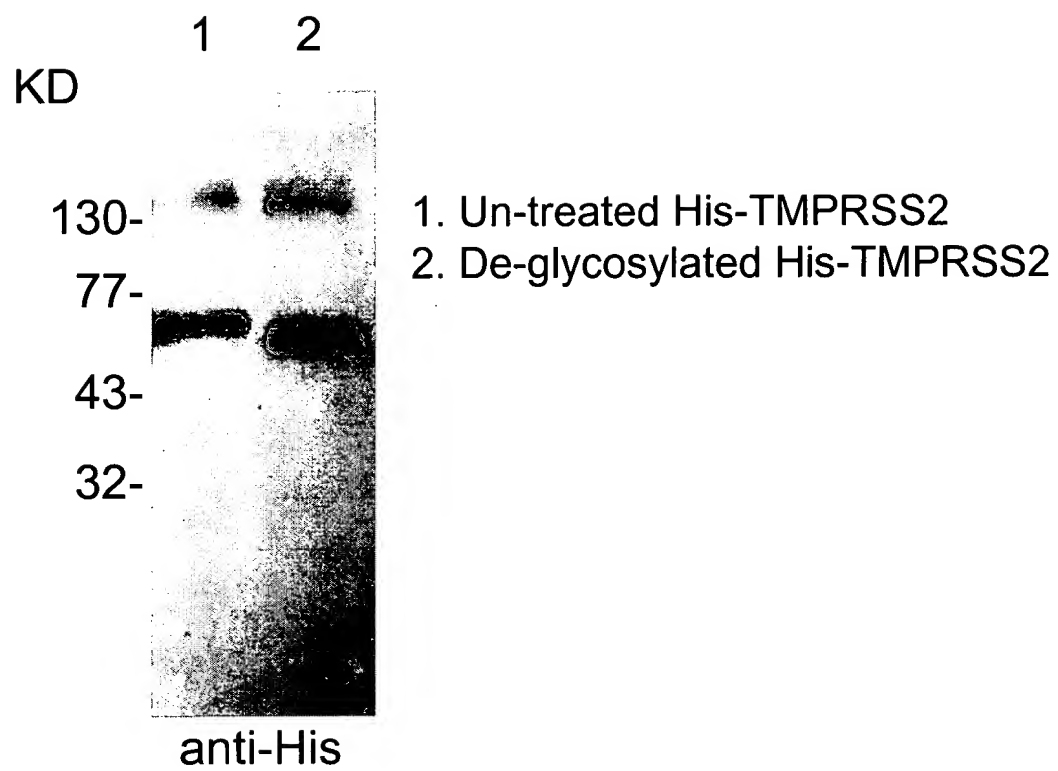
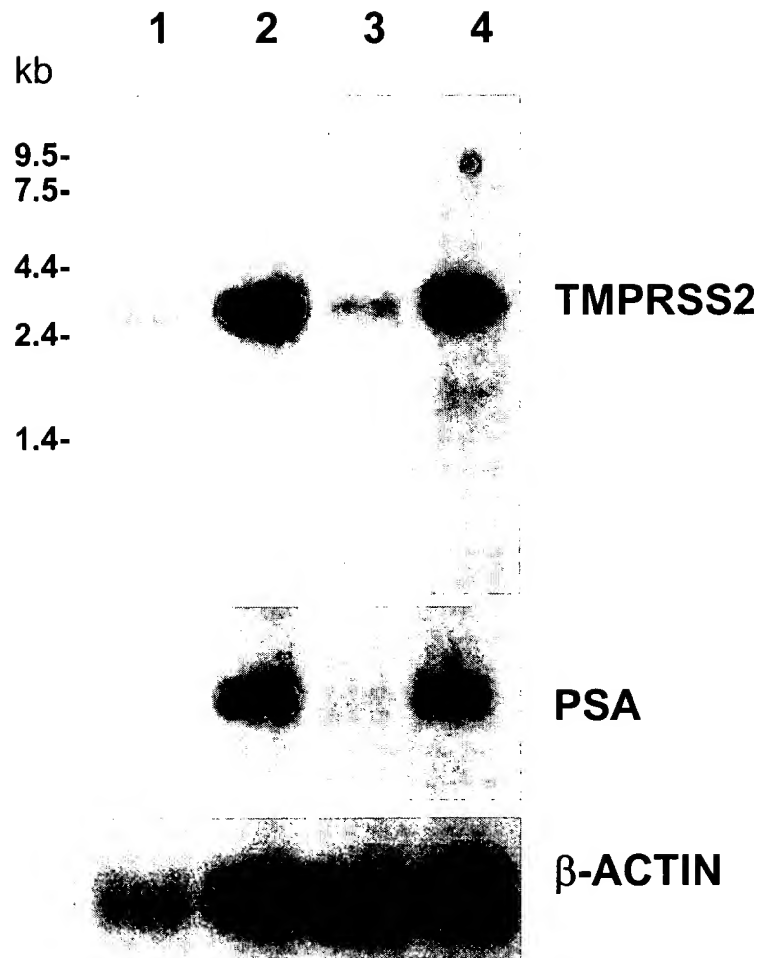


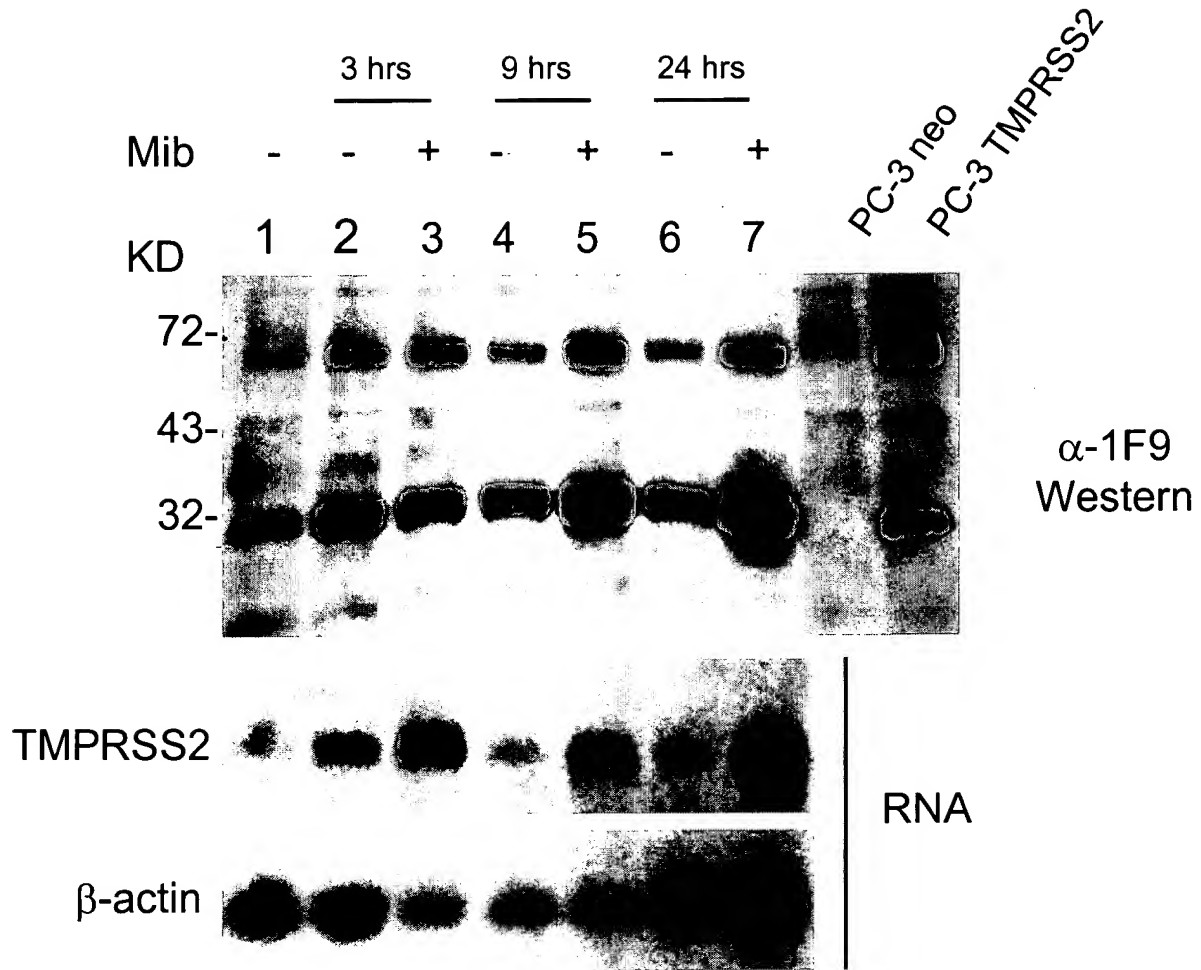
FIG. 11



Panel:

1. LNCaP androgen-deprived 1 week
2. LNCaP FBS
3. LNCaP androgen-deprived 24 hrs + mock 9 hrs
4. LNCaP androgen deprived 24 hrs + Mib 9hrs

FIG. 12

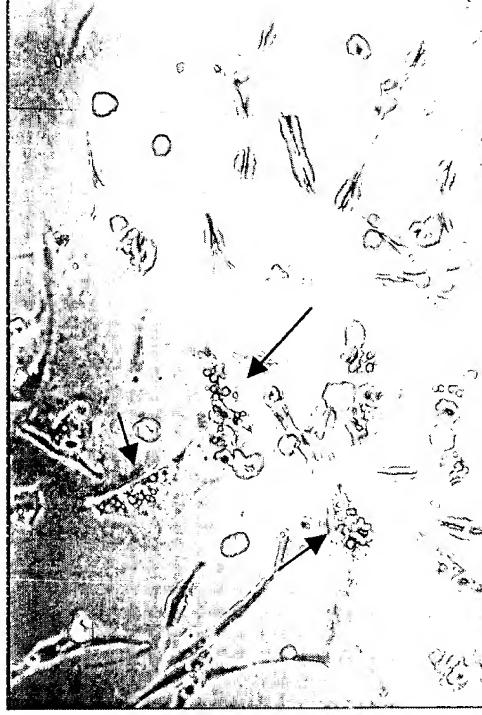


LNCaP cells were androgen deprived for 1 week (grown in 2% CS-FBS) and were then stimulated with 10 nM mibolerone for various time points

FIG. 13



NIH 3T3
neo



NIH 3T3
TMPRSS2

FIG 14

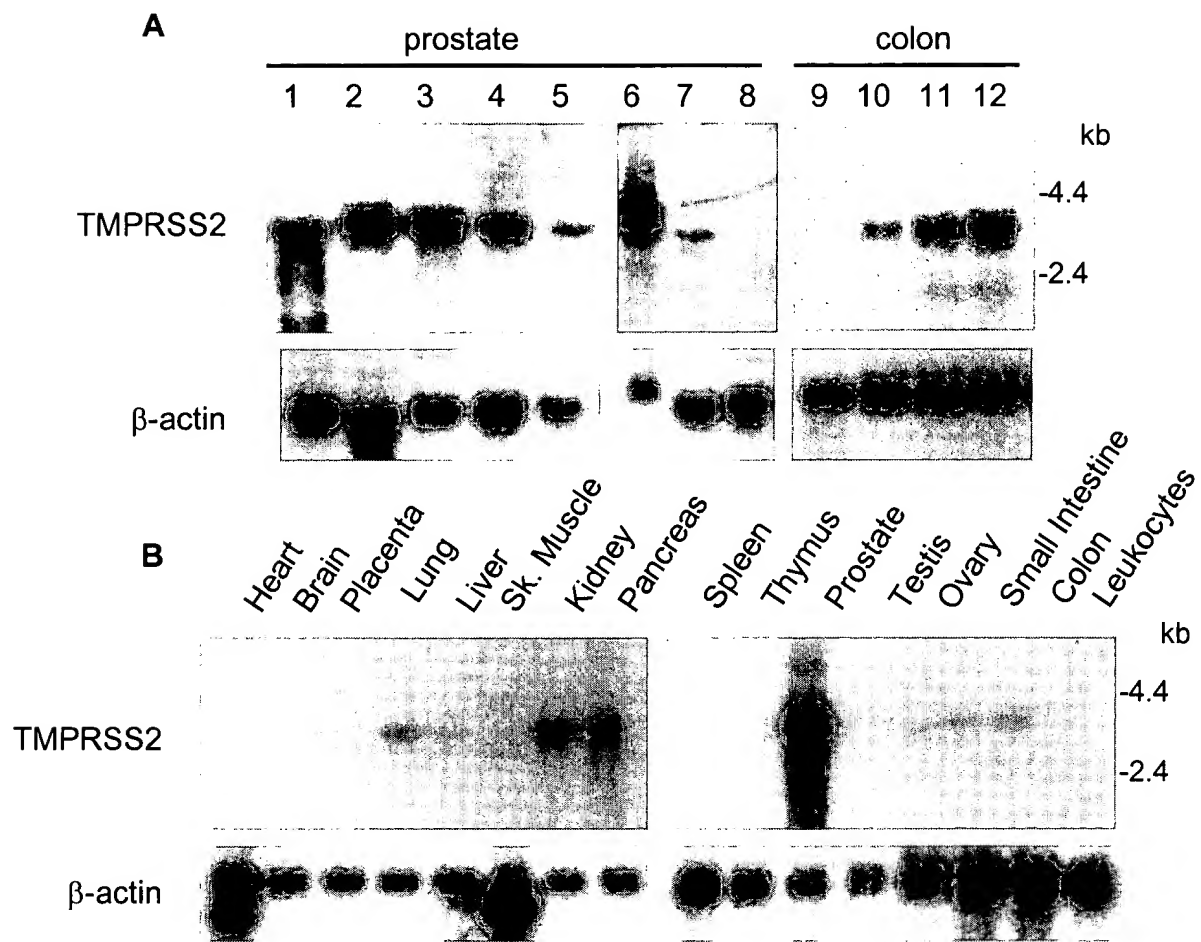


FIG 15

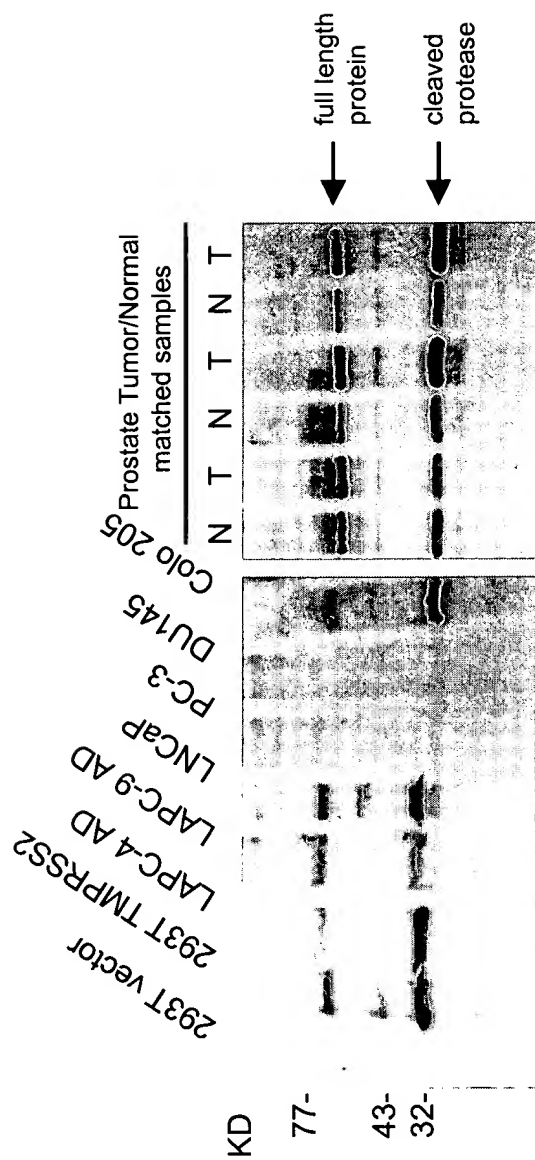
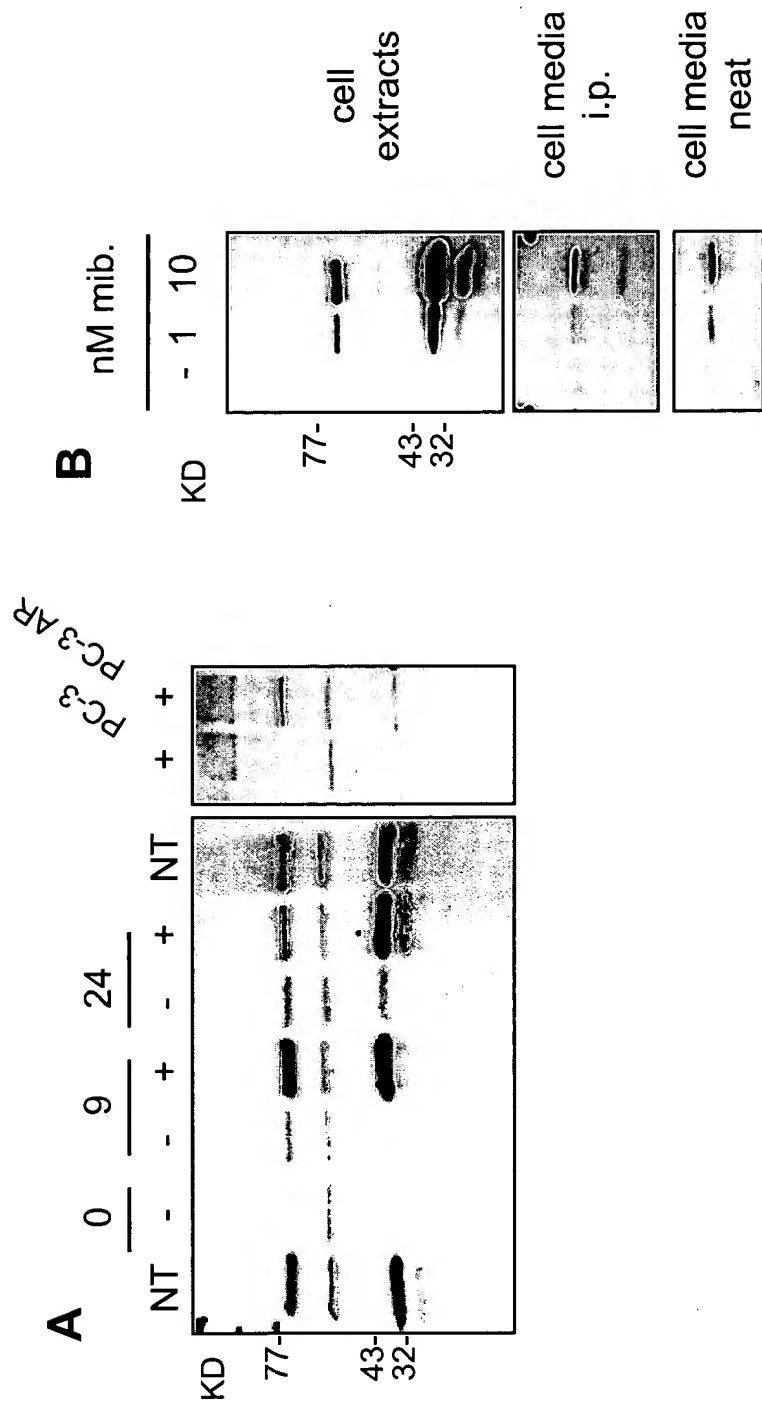


FIG 16



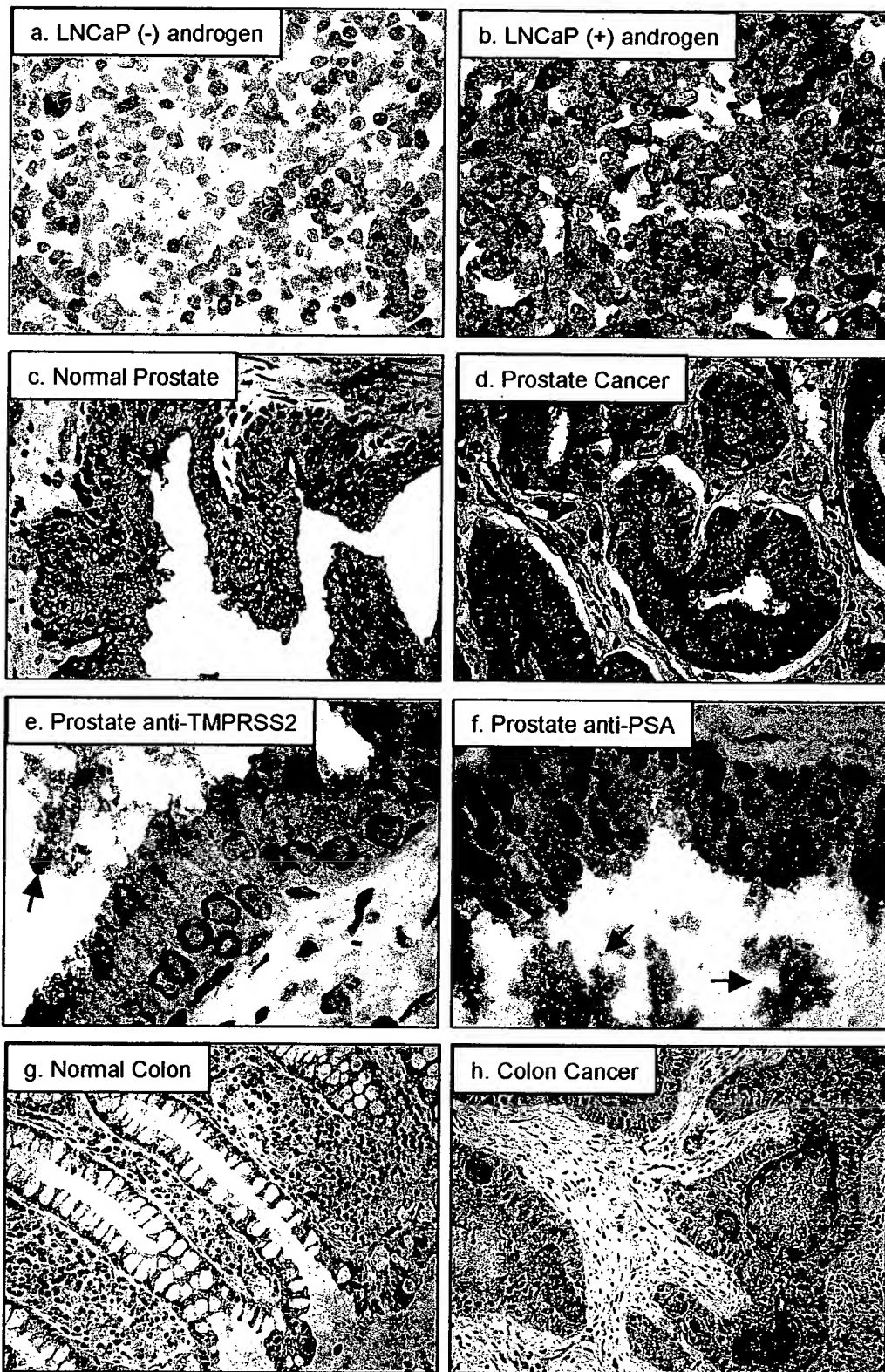


FIG 17

FIG 18

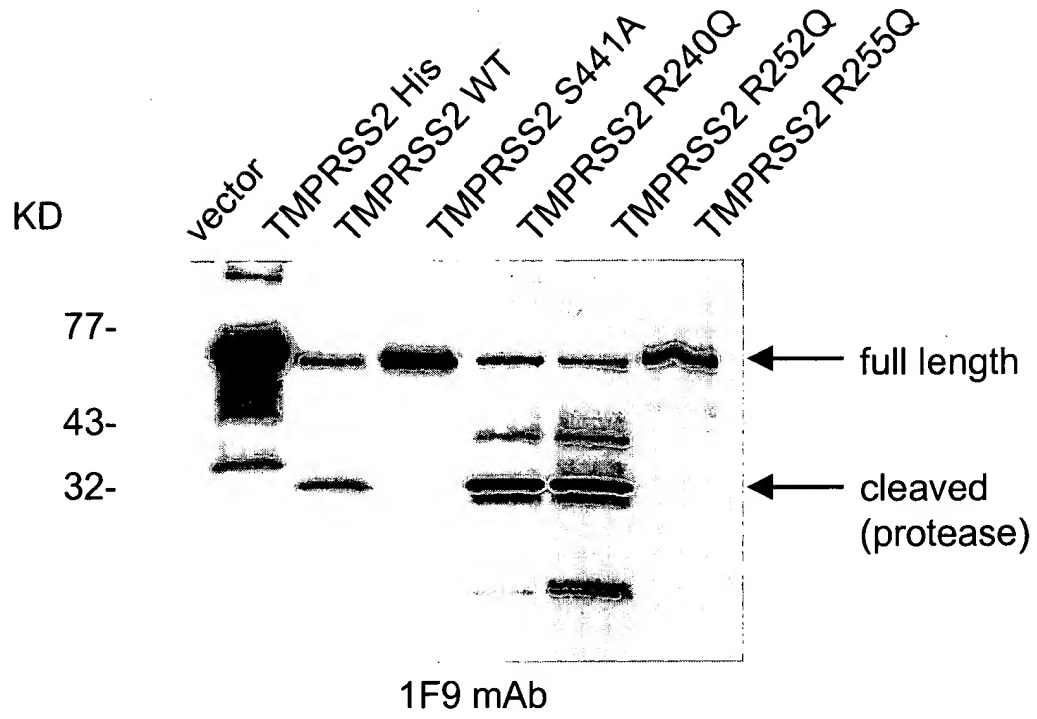


FIG 19

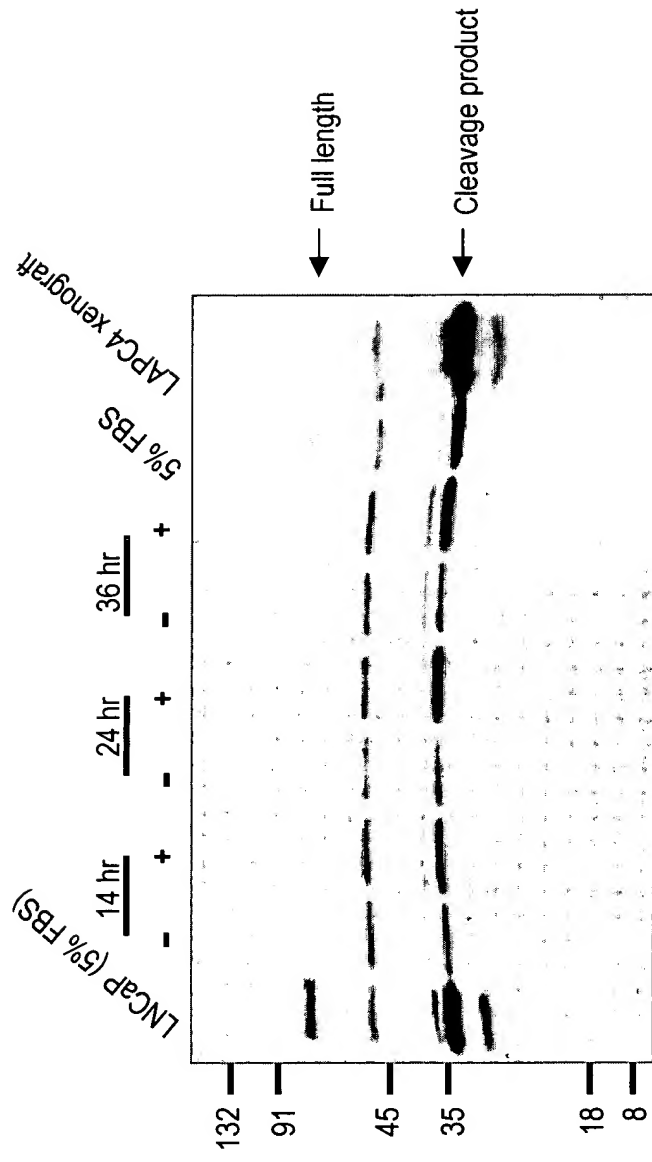
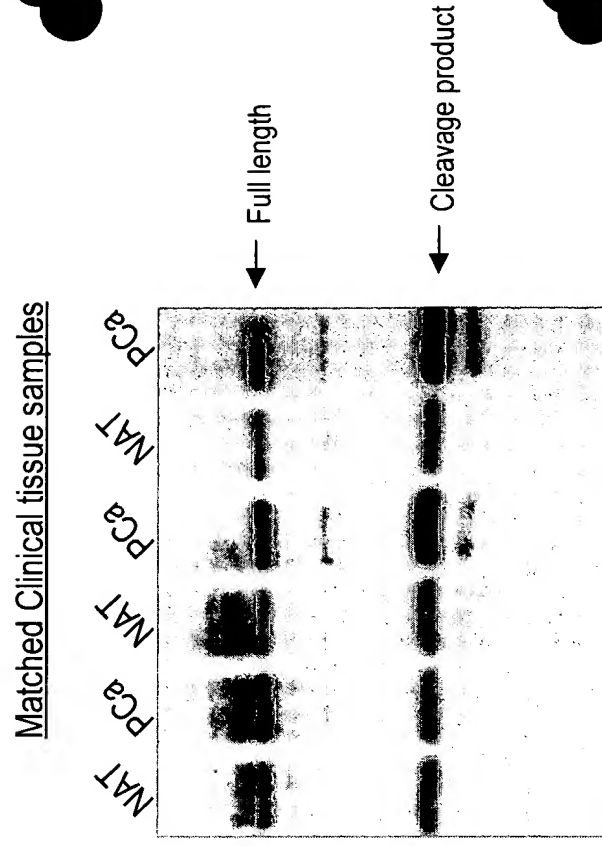
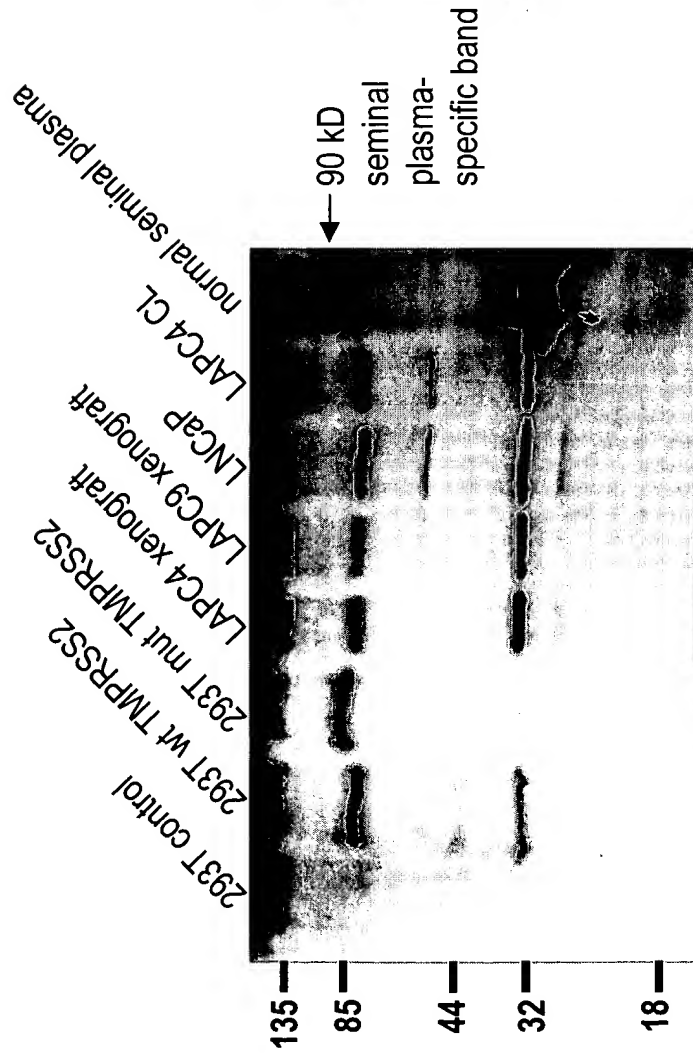


FIG 20



NAT: normal adjacent tissue
PCa: prostate cancer tissue

FIG 21

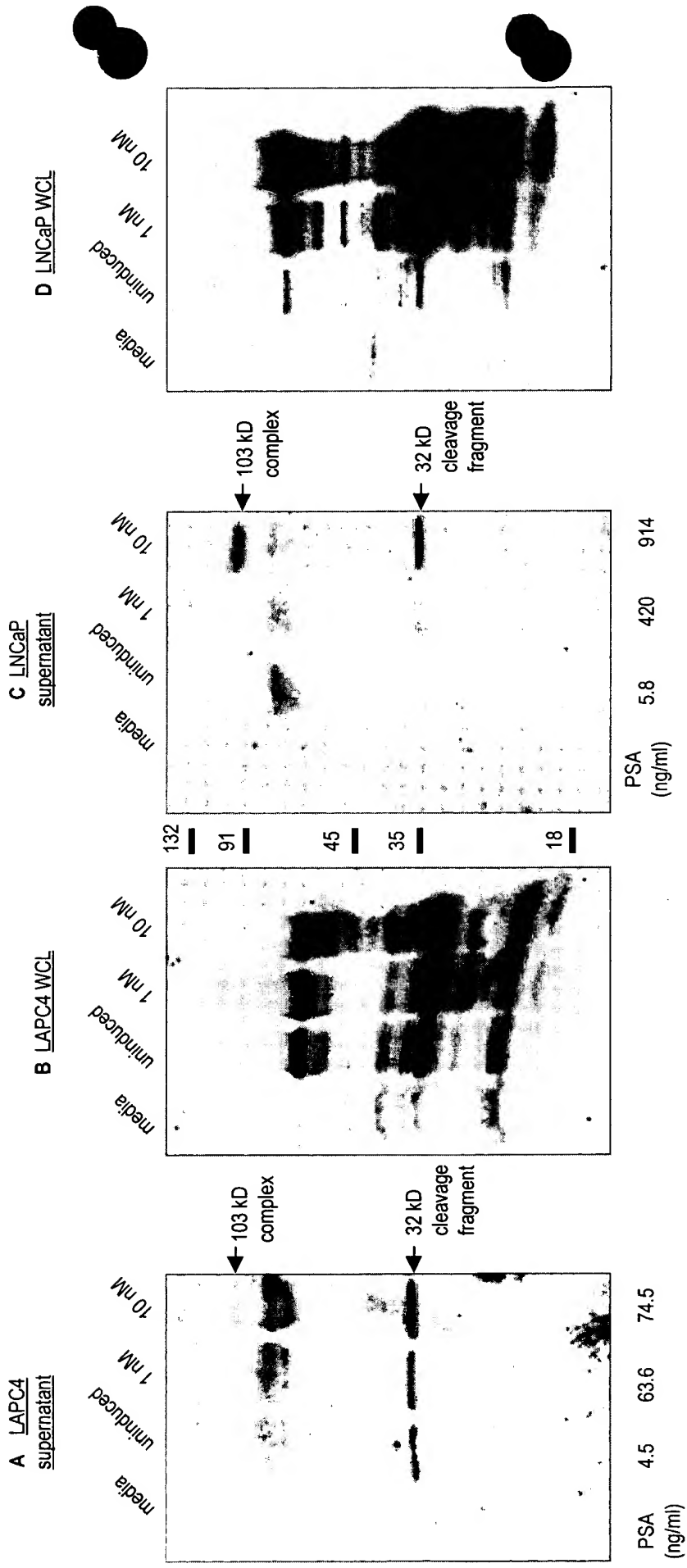


FIG 22

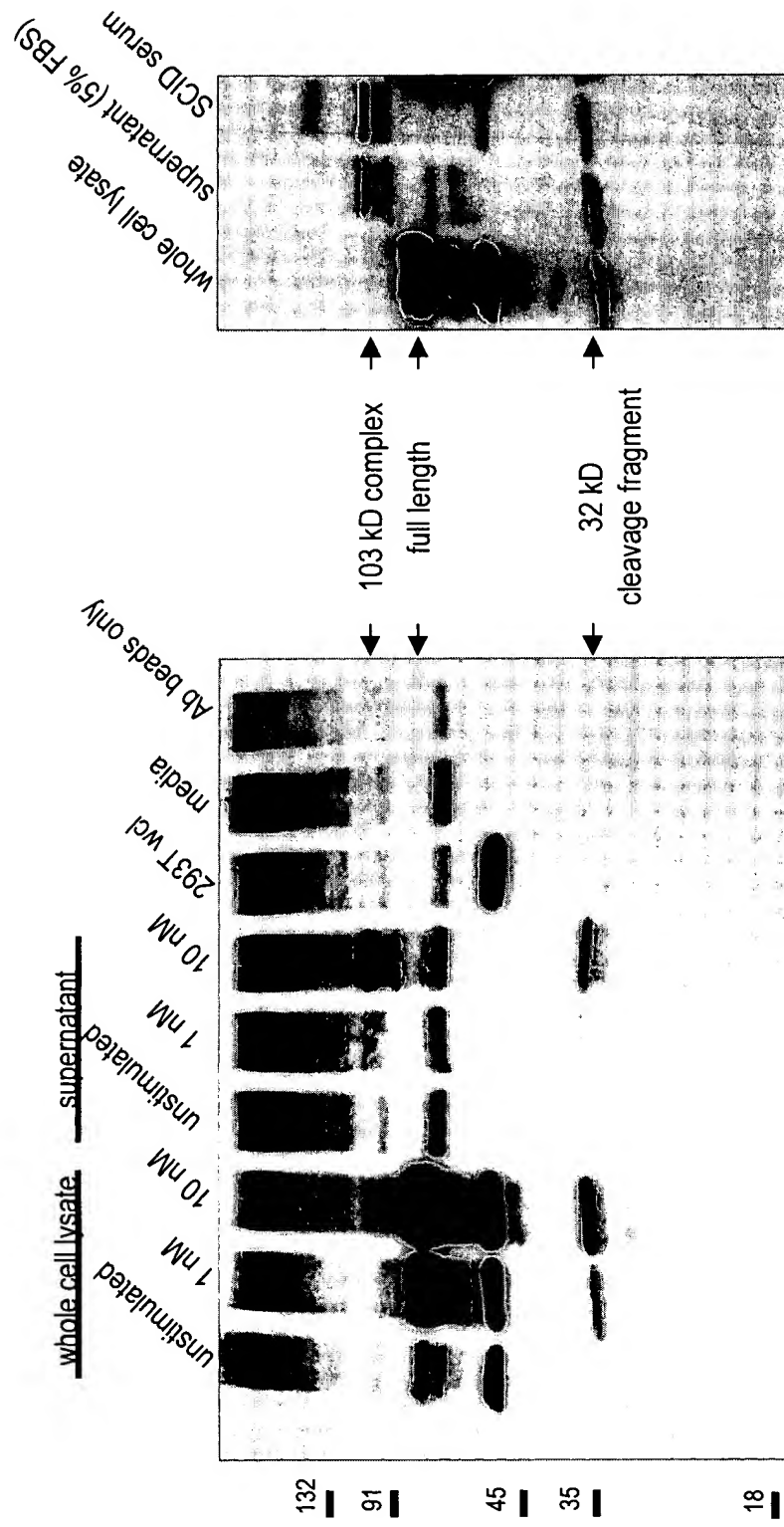


FIG 23

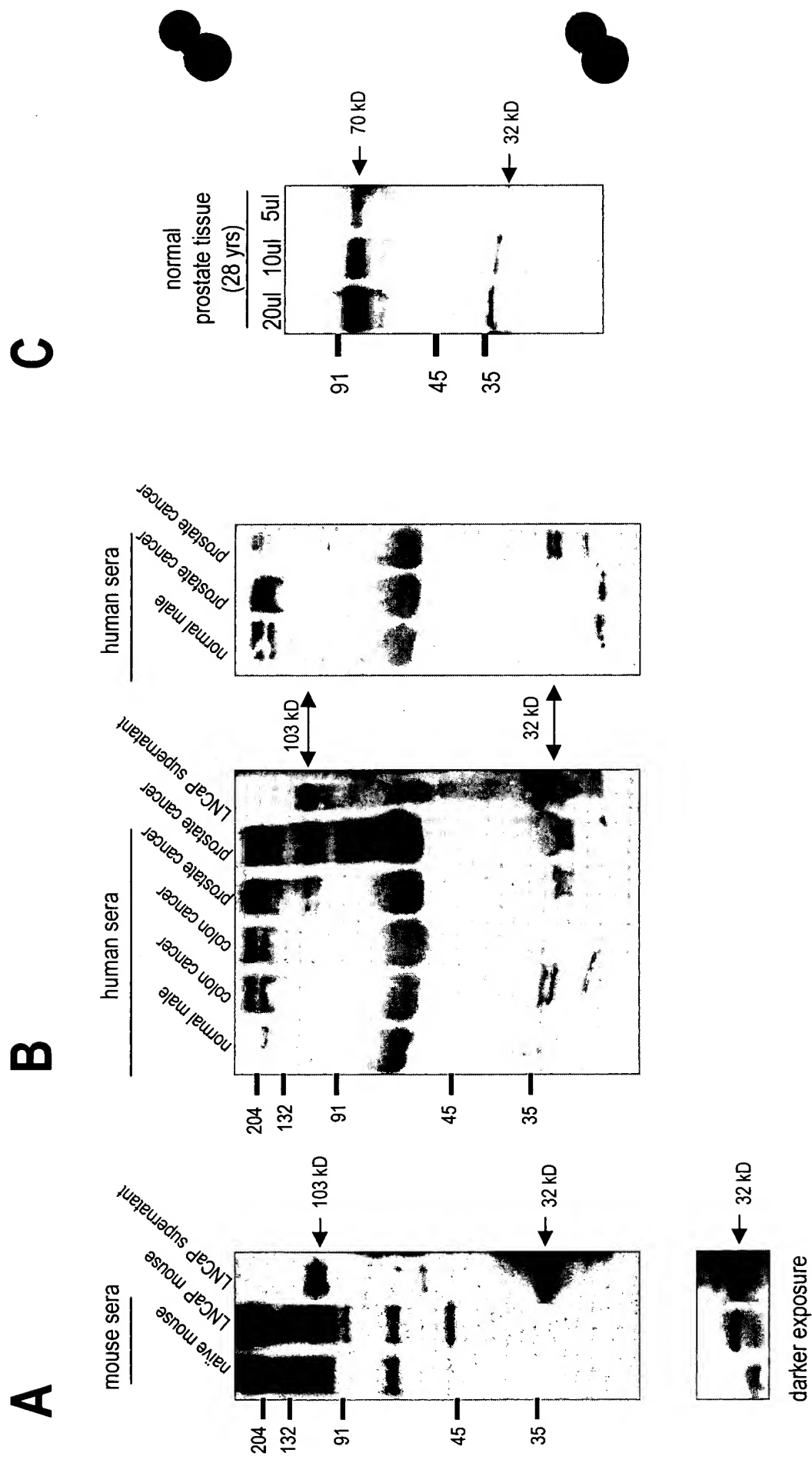


FIG 24

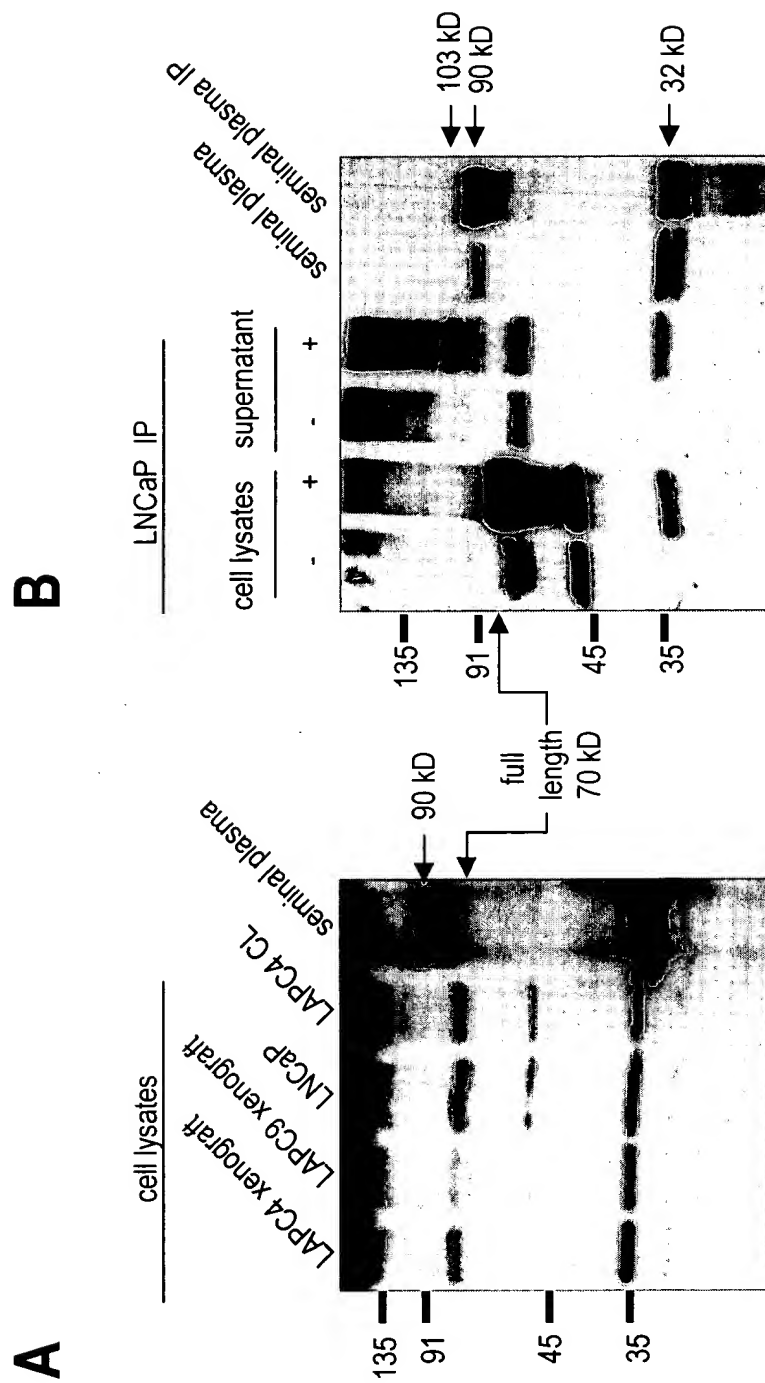


FIG 25

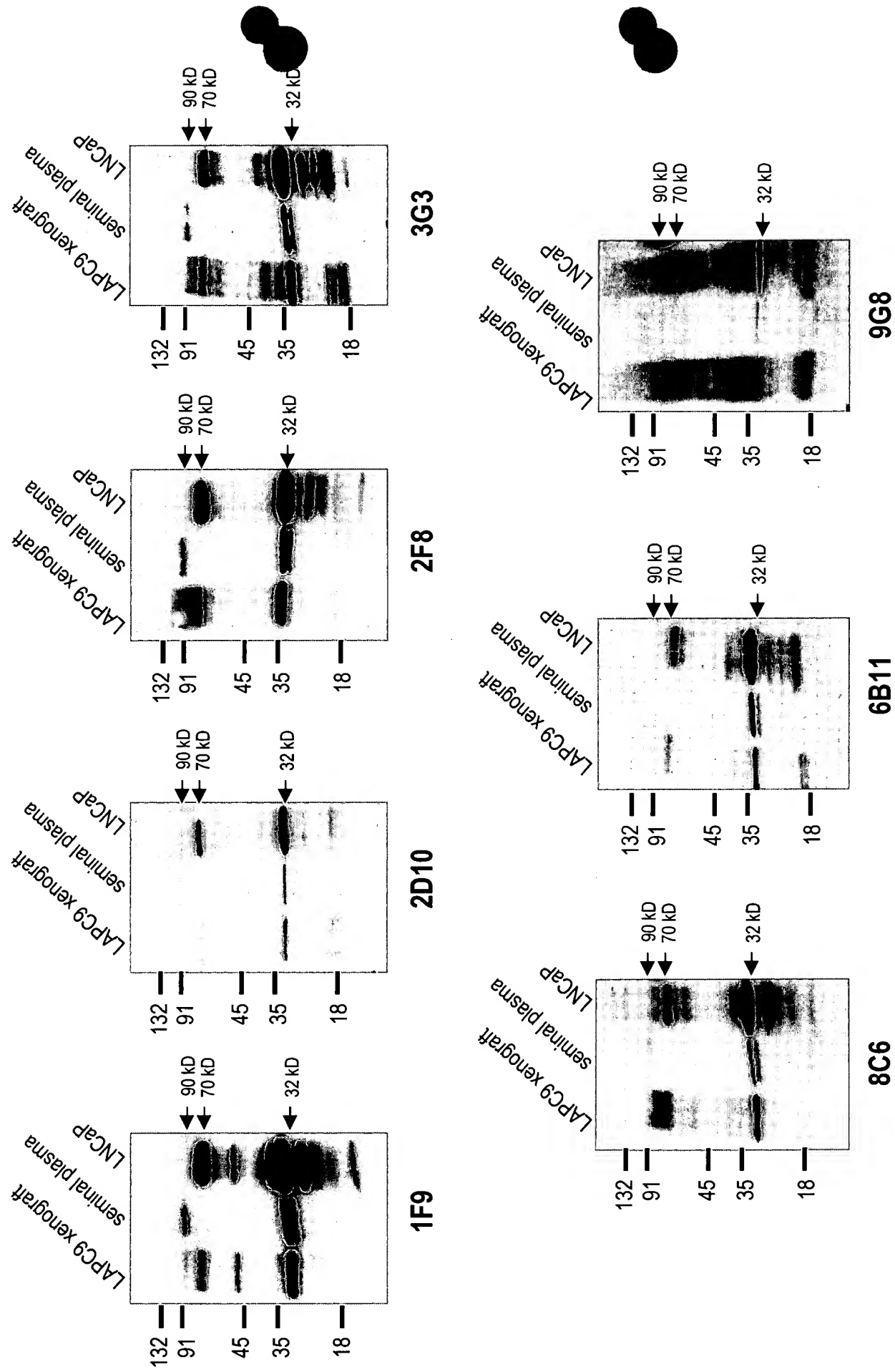


FIG 26

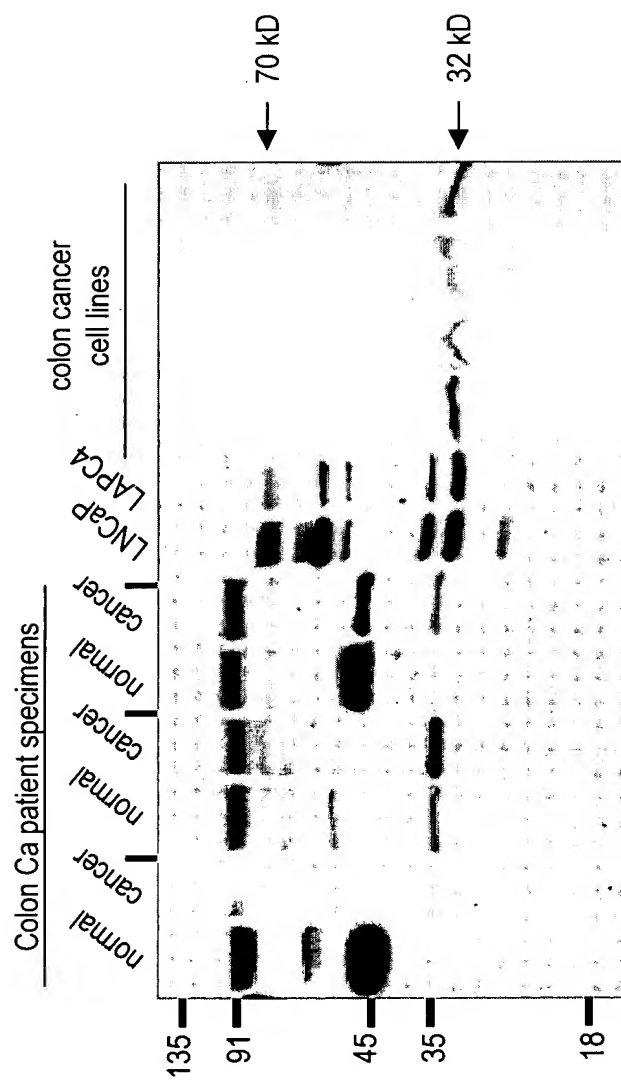


FIG 27A

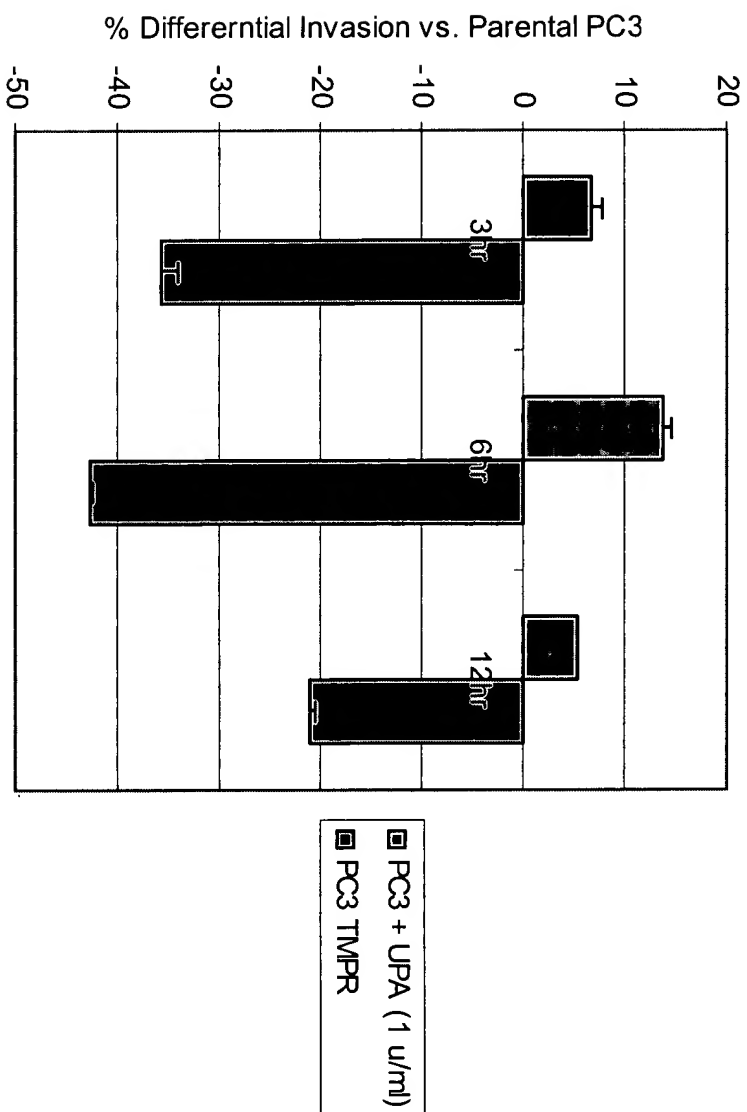


FIG 27B

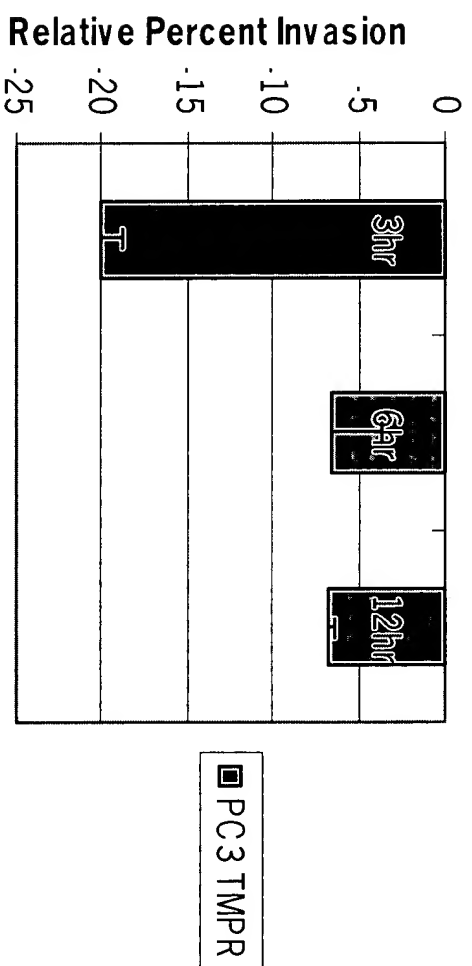


FIG 27C

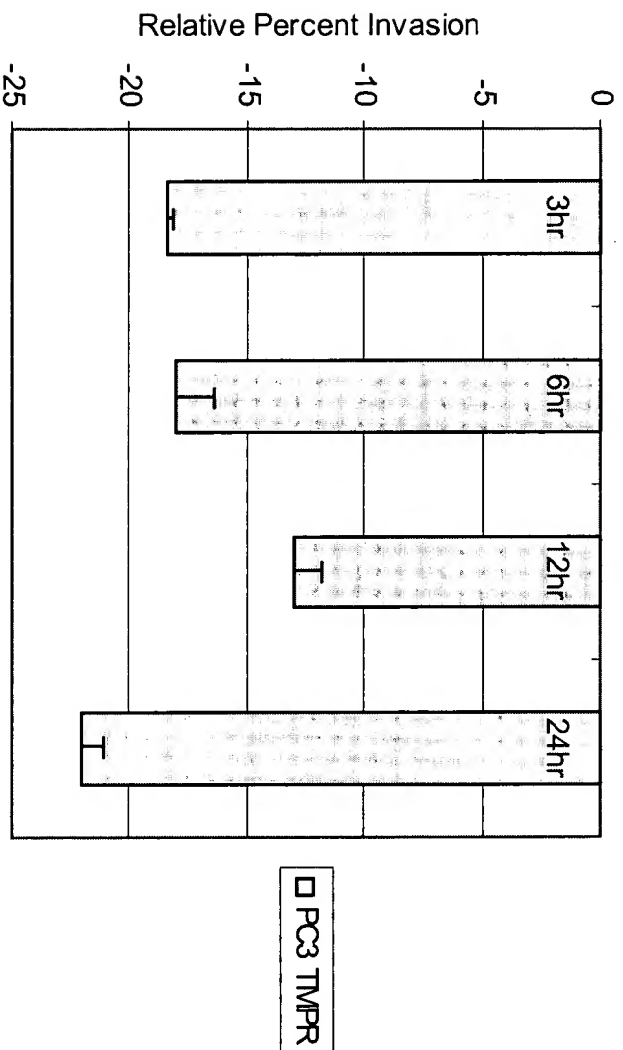


FIG 28

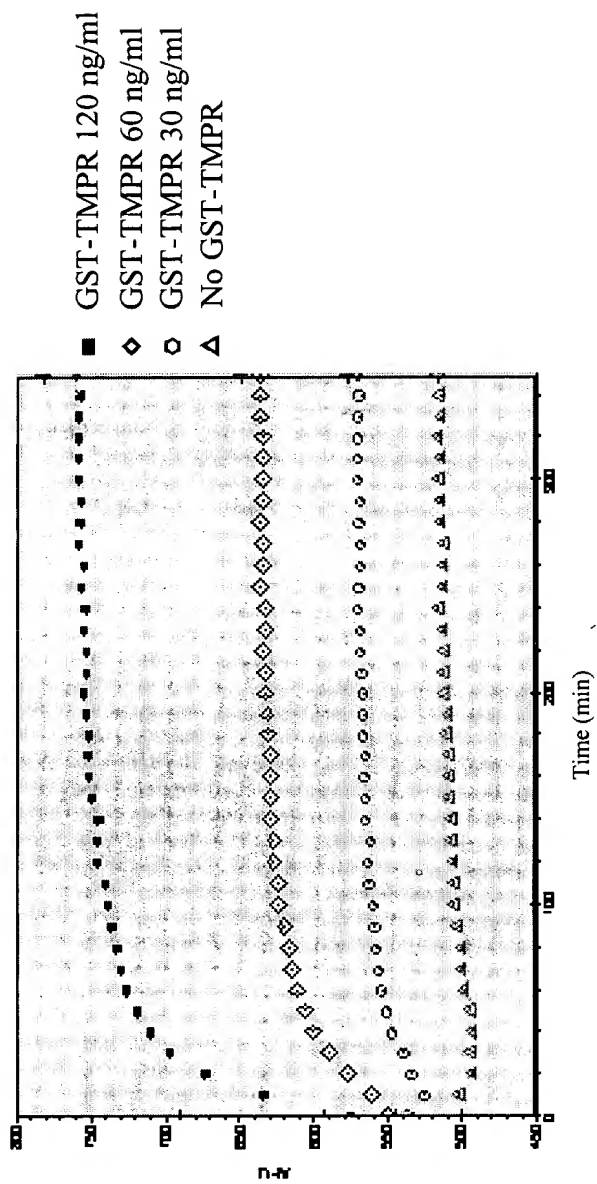


FIG 29

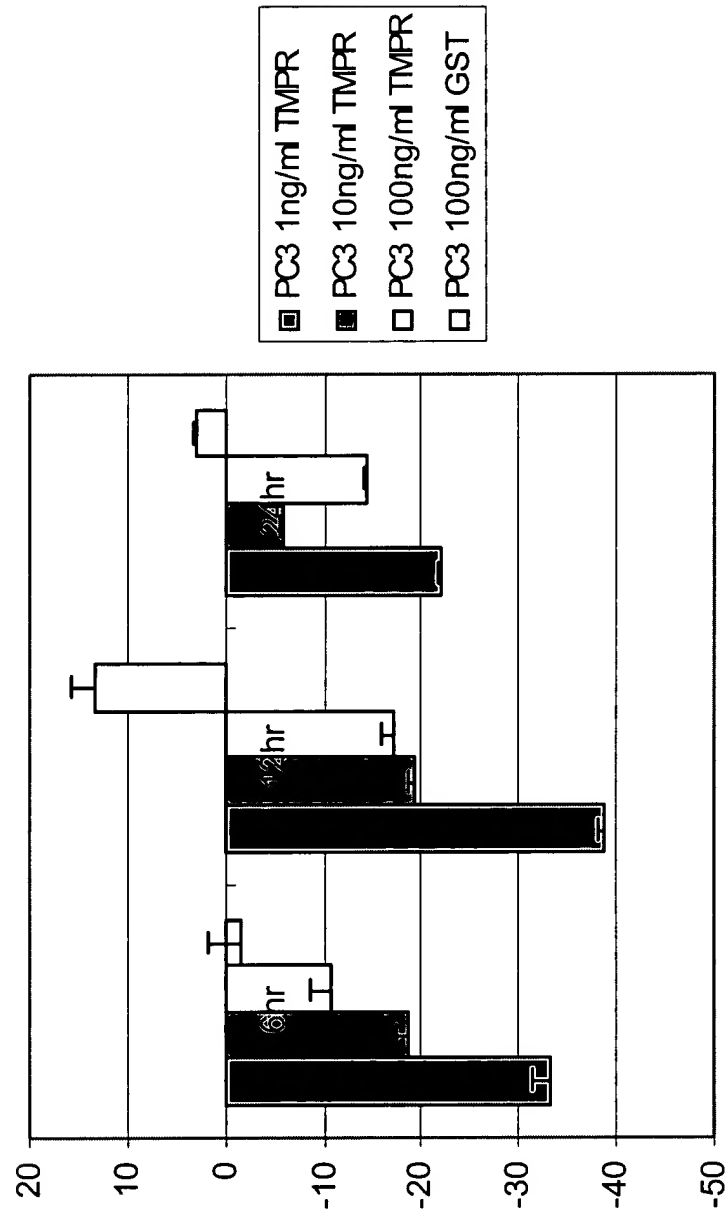


FIG 30

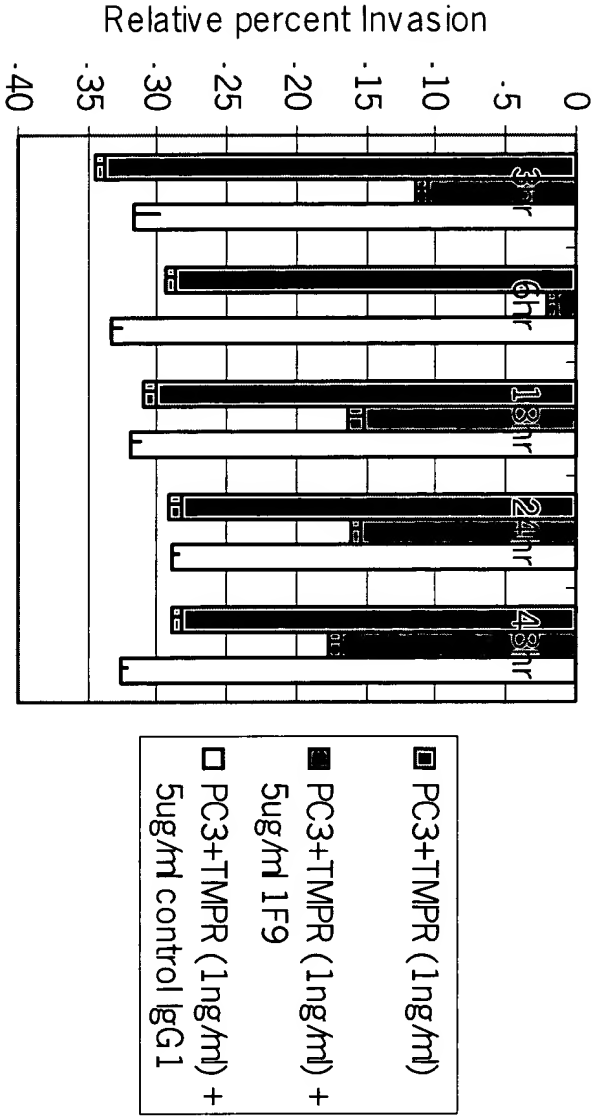
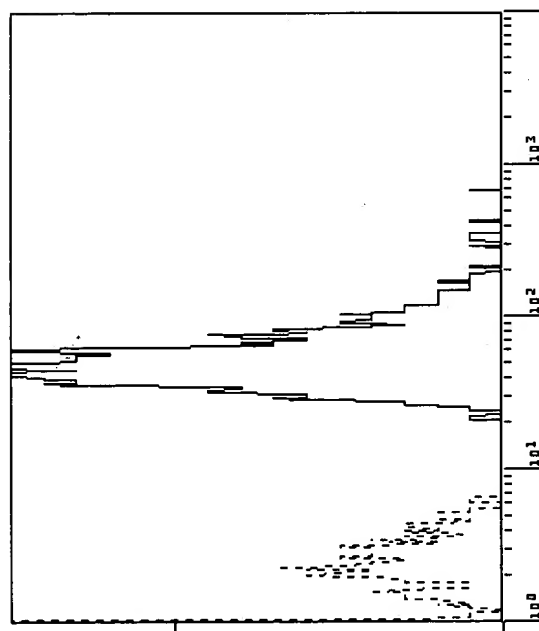


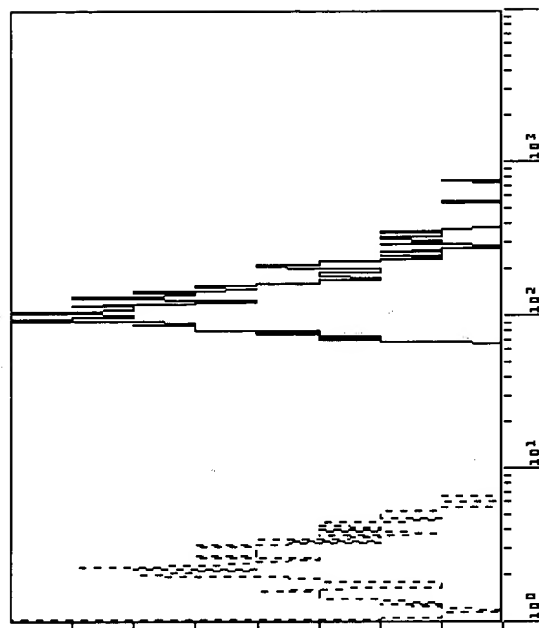
FIG 31

(1):01IC1001.1M0 P11 LOC A



P11 LOC 10uM Morpholino

(1):01IC1006.1M0 P11 LOC A



P11 LOC 30uM Morpholino

FIG 32

